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- (vi) CURRENT APPLICATION DATA:
    - (A) FILING DATE: 14-AUG-1997
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: US60/023931
    - (B) FILING DATE: 14-AUG-1996
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: KATHRYN M. BROWN
    - (B) REGISTRATION NUMBER: 34556
    - (C) REFERENCE/DOCKET NUMBER: 2026-4236PC
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (212) 758-4800
    - (B) TELEFAX: (212) 751-6849
    - (C) TELEX: 421792
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 453 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: No
  - (iv) ANTI-SENSE: No
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCGCGTTG	CTGGCGTTT	TCCATAGGCT	CCGCC	40
GACGAGCATC	ACAAAATCG	ACGCTCAAGT	CAGAGGTGGC	80
GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTTCCCCC	120
TGGAAGCTCC	CTCGTGCCTC	CTCCTGTTCC	GACCCTGCCG	160
CTTACCGGAT	ACCTCTCCGC	CTTTCTCCCT	TCGGGAAGCG	200
TGGCGCTTTC	TCAATGCTCA	CGCIGTAGGT	ATCTCAGTTC	240
GGTGTAGGTC	GTTCGCTCCA	AGCTGGGCTG	TGTGCACGAA	280
CCCCCCGTIC	AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	320
ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	360
ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	400
TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	440
ACTACGGCTA	CAC			453

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 453 base pairs
  - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG	40
CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCAGT	80
GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	120
GACTCAAGAC	GATAGTTACC	GGATAAGGCG	CAGCGGTCGG	160
GCTGAACGGG	GGGTTCGTGC	ACACAGCCC	GCTTGGAGCG	200
AACGACCTAC	ACCGAACTGA	GATACCTACA	CCGTGAGCAT	240
TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	AAGGC GGACA	280
GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	320
GAGGGAGCTT	CCAGGGGAA	ACGCCTGGTA	TCTTTATAGT	360
CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATT	400
TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	440
CAGCAACGCG	GCC			453

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTTTC	GGACTTTGA	AA GTGATGGT	GGTGGCCGAA	40
GGATTGAAAC	CTTCGAAGTC	GATGACGGCA	GATTTAGAGT	80
CTGCTCCCTT	TGGCCGCTCG	GGAACCCCCAC	CACGGGTAAT	120
GCTTTTACTG	GCCTGCTCCC	TTATCAGGGAA	GCGGGGCGCA	160
TCATATCAA	TGACGCGCCG	CTGTAAAGTG	TTACGTTGAG	200
AAAGAATT	C			210

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 209 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

GAATTCTTTC	TCAACGTAAC	ACTTTACAGC	GGCGCGTCAT	40
TTGATATGAT	GCGCCCGCT	TCCCGATAAG	GGAGCAGGCC	80
AGTAAAAGCA	TTACCCGTGG	TGGGGTCCCC	GAGCGGCCAA	120
AGGGAGCAGA	CTCTAAATCT	GCCGTCATCG	ACTTCGAAGG	160
TTCGAATCCT	TCCCCCACCA	CCATCACTTT	CAAAAGTCCG	200
AAAGAATTC				209

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:5:

AATAAA

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:6:

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ATTAAA

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

AGTAAA

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

AAGAAC

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

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(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATACA

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCTTAAGGG	CCATATGGTG	AGTGGATCCC	TTGACCCAG	40
GCAGGGATGG	GGAGACCTG	TAGTCAGAGC	CCCCGGGCAG	80
CACAGGCCAA	TGCCCCGTCT	TCCCCTGCAG	GATGAGTAGT	120
GAGTGCCTCT	CCTGGCCCTG	GAAGTTGCCA	CTCCAGTGCC	160
CACCAGCCTT	GTCCTAATAA	AATTAAGTTG	CATCATTTG	200
TCTGACTAGG	TGTCCCTCAT	AATATTAT		228

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAATATTAT	AGAGGACACC	TAGTCAGAAC	AAATGATGCA	40
ACTTAATTTC	ATTAGGACAA	GGCTGGTGGG	CACTGGAGTG	80
GCAACTTCCA	GGGCCAGGAG	AGGCACTCAC	TACTCATCCT	120

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GCAGGGGAAG GACGGGCATT GGCCTGTGCT GCCCGGGGGC TCTGACTACA GGTCTCCCCC ATCCCCGCCT GGGGTCAAGG CATCCACTCA CCATATGGCC CTTAAGG	160 200 228
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## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 252 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

CCTCGGTACC TGCCATGGCG CGGATTCTTT ATCACTGATA AGTTGGTCCA CATATTATGT TTATCAGTGA TAAAGTGTCA AGCATGACAA AGTTGCAGCC GAATACAGTG ATCCGTGCCG GCCCTGGACT GTTGAACGAG GTCGGCGTAG ACGGTCTGAC GACACGCAA CTGGCGGAAC GGTTGGGGGT GCAGCAGCCG GCGCTTTACT GGCACTTCAAG GAACAAGCGG GCGCCTTAAG GGCCATATGC CG	40 80 120 160 200 240 252
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## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

CCTCGGTACC TGCCACCATG GCGCGGATTC TTTAT	35
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## (2) INFORMATION FOR SEQ ID NO:14:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGCATATGG CCTTAAGGCG CCCGCTTGTT CCTGAAGT

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 228 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTTAAGGG	CCATATGGTG	AGTGGATGCC	TTGACCCCAG	40
GCGGGGATGG	GGGAGACCTG	TAGTCAGAGC	CCCCGGGCAG	80
CACAGGCCAA	TGCCCCGTCT	TCCCCTGCAG	GATGAGTAGT	120
GAGTGCCTCT	CCTGGCCCTG	GAAGTTGCCA	CTCCAGTGCC	160
CACCAGCCTT	GTCCTAATAA	AATTAAGTTG	CATCATTTG	200
TCTGACTAGG	TGTCCCTCTAT	AATATTAT		228

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1425 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCCATGGCG	CGGATTCTTT	ATCACTGATA	AGTTGGTGGAA	40
CATATTATGT	TTATCAGTGA	TAAAGTGTCA	AGCATGACAA	80
AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	GCCCTGGACT	120
GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	GACACGCAA	160
CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	GCGCTTTACT	200
GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	GGCCATATGG	240
TGAGTGGATG	CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	280
TGTAGTCAGA	GCCCCCGGGC	AGCACAGGCC	AATGCCCGTC	320
CTTCCCCTGC	AGTGAGTAGT	GAUTGCCCGG	GTGGGATCCC	360
TGTGACCCCT	CCCCAGTGCC	TCTCCTGGCC	CTGGAAGTTG	400
CCACTCCAGT	GCCCCACCAGC	CTTGTCTCAA	TAAAATTAAG	440
TTGCATCATT	TTGTCTGACT	AGGTGTCTC	TATAATATTA	480
TAAGCTTGAT	ATCGAATTCT	TTCTCAACGT	AACACTTAC	520
AGCGGCGCGT	CATTTGATAT	GATGCGCCCC	GCTTCCCGAT	560
AAGGGAGCAG	GCCAGTAAAA	GCATTACCCG	TGGTGGGGTT	600
CCCGAGCGGC	CAAAGGGAGC	AGACTCTAAA	TCTGCCGTCA	640
TCGACTTCGA	AGGTTCGAAT	CCTTCCCCCA	CCACCATCAC	680
TTTCAAAAGT	CCGAAAGAAT	TCCTGCAGCC	CGTGTAGCCG	720
TAGTTAGGCC	ACCACTCAA	GAACCTCTGTA	GCACCGCCTA	760
CATACCTCGC	TCTGCTAAC	CTGTTACCAG	TGGCTGCTGC	800
CAGTGGCGAT	AAAGTCGTGTC	TTACCGGGTT	GGACTCAAGA	840
CGATAGTTAC	CGGATAAGGC	GCAGCGGTG	GGCTGAACGG	880
GGGGTTCGTG	CACACAGCCC	AGCTTGGAGC	GAACGACACTA	920
CACCGAACTG	AGATAACCTAC	AGCGTGAGCA	TTGAGAAAGC	960
GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	1000
TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	1040
TCCAGGGGGA	AACGCCTGGT	ATCTTTATAG	TCCTGTCCGG	1080
TTTCGCCACC	TCTGACTTGA	CGTCGATTT	TTGTGATGCT	1120
CGTCAGGGGG	GCGGAGCCTA	TGGAAAAACG	CCAGCAACGC	1160
GGCCGGGGGA	TCCGGAGAGC	TCACTCTAGA	TGAGAGAGCA	1200
GTGAGGGAGA	GACAGAGACT	CGAATTCCG	GAGCTATTT	1240
AGTTTTCTTT	TCCGTTTTGT	GCAATTTCAC	TTATGATACC	1280
GGCCAATGCT	TGGTTGCTAT	TTTGGAAACT	CCCCTTAGGG	1320
GATGCCCTC	AACTGGCCCT	ATAAAAGGGCC	AGCCTGAGCT	1360
GCAGAGGATT	CCTGCAGAGG	ATCAAGACAG	CACGTGGACC	1400
TCGCACAGCC	TCTCCCACAG	GTACC		1425

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

ATGAGCAAG	GGCGAGGAAC	TGTTCACTGG	CGTGGTCCCA	40
ATTCTCGTGG	AACTGGATGG	CGATGTGAAT	GGGCACAAAT	80
TTTCTGTCAG	CGGAGAGGGT	GAAGGTGATG	CCACATACGG	120
AAAGCTCACC	CTGAAATTCA	TCTGCACCAAC	TGGAAAGCTC	160
CCTGTGCCAT	GGCCAACACT	GGTCACTACC	TTCACCTATG	200
GCGTGCAGTG	CTTTTCCAGA	TACCCAGACC	ATATGAACGA	240
GCATGACTTT	TTCAAGAGCG	CCATGCCCGA	GGGCTATGTG	280
CAGGAGAGAA	CCATCTTTT	CAAAGATGAC	GGGAACATACA	320
AGACCCCGCGC	TGAAGTCAAG	TTCGAAGGTG	ACACCCCTGGT	360
GAATAGAACATC	GAGTTGAAGG	GCATTGACTT	TAAGGAAGAT	400
GGAAACATTC	TCGGCCACAA	GCTGGAATAC	AACTATAACT	440
CCCACAAATGT	GTACATCATG	GCCGACAAAGC	AAAAGAATGG	480
CATCAAGGTC	AACTTCAAGA	TCAGACACAA	CATTGAGGAT	520
GGATCCGTGC	AGCTGGCCGA	CCATTATCAA	CAGAACACTC	560
CAATCGGCAGA	CCGCCCTGTG	CTCCTCCAG	ACAACAAATTA	600
CCTGTCCACC	CAGTCTGCC	TGTCTAAAGA	TCCCAACGAA	640
AAGAGAGAGACC	ACATGGTCCT	GCTGGAGTTT	GTGACCGCTG	680
CTGGGATCAC	ACATGGCATG	GACGAGCTGT	ACAAGTGAGC	720

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1911 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:

TATGAGCAAG	GGCGAGGAAC	TGTTCACTGG	CGTGGTCCCA	40
ATTCTCGTGG	AACTGGATGG	CGATGTGAAT	GGGCACAAAT	80
TTTCTGTCAG	CGGAGAGGGT	GAAGGTGATG	CCACATACGG	120
AAAGCTCACC	CTGAAATTCA	TCTGCACCAAC	TGGAAAGCTC	160
CCTGTGCCAT	GGCCAACACT	GGTCACTACC	TTCACCTATG	200
GCGTGCAGTG	CTTTTCCAGA	TACCCAGACC	ATATGAAGCA	240
GCATGACTTT	TTCAAGAGCG	CCATGCCCGA	GGGCTATGTG	280

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CAGGAGAGAA	CCATTTTTT	CAAAGATGAC	GGGAACTACA	320
AGACCCCGCGC	TGAAGTCAAG	TTCGAAGGTG	ACACCCTGGT	360
GAATAGAATC	GAGTTGAAGG	GCATTGACTT	TAAGGAAGAT	400
GGAAACATTC	TCGGCCACAA	GCTGGAATAC	AACTATAACT	440
CCCACAATGT	GTACATCATG	GCCGACAAGC	AAAAGAATGG	480
CATCAAGGTC	AACTTCAAGA	TCAGACACAA	CATTGAGGAT	520
GGATCCGTGC	AGCTGGCCGA	CCATTATCAA	CAGAACACTC	560
CAATCGGCGA	CGGCCCTGTG	CTCCTCCCAG	ACAACCATTA	600
CCTGTCCACC	CAGTCTGCC	GTCTAAAGAT	CCCAACGAAA	640
AGAGAGACCA	CATGGTCCTG	CTGGAGTTG	TGACCGCTGC	680
TGGGATCACA	CATGGCATGG	ACGAGCTGTA	CAAGTGAGCC	720
ATATGGTGAG	TGGATGCCTT	GACCCCAGGC	GGGGATGGGG	760
GAGACCTGTA	GTCAGAGCCC	CCGGGCAGCA	CAGGCCAATG	800
CCCGTCCCTC	CCCTGCAGTG	AGTAGTGA	GCCCCGGTGG	840
GATCCCTGTG	ACCCCTCCCC	AGTGCCTCTC	CTGGCCCTGG	880
AAGTTGCCAC	TCCAGTGC	ACCAGCCTTG	TCCTAATAAA	920
ATTAAGTTGC	ATCATTG	CTGACTAGGT	GTCCTCTATA	960
ATATTATAAG	CTTGATATCG	AATTCTTCT	CAACGTAACA	1000
CTTTACAGCG	GCGCGTCATT	TGATATGATG	CGCCCCGCTT	1040
CCCGATAAGG	GAGCAGGCCA	GTAAAAGCAT	TACCCGTGGT	1080
GGGGTCCCCG	AGCGGCCAAA	GGGAGCAGAC	TCTAAATCTG	1120
CCGTCATCGA	CTTCGAAGGT	TCGAATCCTT	CCCCCACAC	1160
CATCACTTTC	AAAAGTCCGA	AAGAATTCC	GCAGCCGTG	1200
TAGCCGTAGT	TAGGCCACCA	CTTCAAGAAC	TCTGTAGCAC	1240
CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCACTGGC	1280
TGCTGCCAGT	GGCGATAAGT	CGTGTCTTAC	CGGGTTGGAC	1320
TCAAGACGAT	AGTTACCGGA	TAAGGCGCAG	CGGTCGGGCT	1360
GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	1400
GACCTACACC	GAACGTGAGAT	ACCTACAGCG	TGAGCATTGA	1440
GAAAGCGCCA	CGCTTCCC	AGGGAGAAAG	CGGGACAGGT	1480
ATCCGGTAAG	CGGCAGGGTC	GGAACAGGG	AGCGCACGAG	1520
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	1560
GTCGGGTTTC	GCCACCTCTG	ACTTGAGCGT	CGATTTTGT	1600
GATGCTCGTC	AGGGGGCGG	AGCCTATGGA	AAAACGCCAG	1640
CAACCGGGCC	GGGGGATCCG	GAGAGCTCAC	TCTAGATGAG	1680
AGAGCAGTGA	GGGAGAGACA	GAGACTCGAA	TTTCCGGAGC	1720
TATTCAGTT	TTCTTTCCG	TTTTGTGCAA	TTTCACTTAT	1760
GATACCGGCC	AATGCTTGGT	TGCTATTTG	GAAACTCCCC	1800
TTAGGGGATG	CCCCTCAACT	GGCCCTATAA	AGGGCCAGCC	1840
TGAGCTGCAG	AGGATTCCTG	CAGAGGATCA	AGACAGCACG	1880
TGGACCTCGC	ACAGCCTCTC	CCACAGGTAC	C	1911

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:19:

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Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro  
1 5 10  
Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn  
15 20  
Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly  
25 30 35  
Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser  
40 45  
Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val  
50 55 60  
Val Leu Gly Val Val Phe Gly Ile Leu  
65

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 287 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:

Pro Ala Pro Gly Ala Gly Gly Met Val His His Arg  
1 5 10  
His Arg Ser Ser Ser Thr Arg Ser Gly Gly Gly Asp  
15 20  
Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Ala  
25 30 35  
Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly  
40 45  
Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala  
50 55 60  
Ala Lys Gly Leu Ser Leu Pro Thr His Asp Pro Ser  
65 70  
Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro  
75 80  
Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu  
85 90 95  
Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro  
100 105  
Asp Val Arg Pro Pro Pro Ser Pro Arg Glu Gly Pro  
110 115 120  
Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu  
125 130  
Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val  
135 140

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Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu  
145 150 155  
Asn Pro Glu Tyr Leu Thr Pro Gln Gly Thr Cys Ser  
160 165  
Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg  
170 175 180  
Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro  
185 190  
Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro  
195 200  
Lys Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp  
205 210 215  
Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu  
220 225  
Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro  
230 235 240  
His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn  
245 250  
Leu Tyr Tyr Trp Asp Asp Pro Pro Glu Arg Gly Ala  
255 260  
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu  
260 270 275  
Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val  
280 285

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:

Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val  
1 5 10  
Val Leu Gly Val Val Phe Gly Ile Leu Ile  
15 20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2145 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:22:

GCCACCATGG	CCCCTGACCT	CTCCTACATG	CCCATCTGGA	40
AGTTTCCAGA	TGAGGAGGGC	GCATGCCAGC	CTTGCCCCAT	80
CAACTGCACC	CACTCCTGTG	TGGACCTGGA	TGACAAGGGC	120
TGCCCGGCCG	AGCAGAGAGC	CAGCCCTCTG	ACGTCCATCA	160
TCTCTGCGGT	GGTTGGCATT	CTGCTGGTCG	TGGTCTTGGG	200
GGTGGTCTTT	GGGATCCTCA	TCAAGCGACG	GCAGCAGAAAG	240
ATCACATGTC	CAGACCCTGC	CCCGGGCGCT	GGGGGCATGG	280
TCCACCACAG	GCACCGCAGC	TCATCTACCA	GGAGTGGCGG	320
TGGGGACCTG	ACACTAGGGC	TGGAGCCCTC	TGAAGAGGAG	360
GCCCCCAGGT	CTCCACTGGC	ACCCTCCGAA	GGGGCTGGCT	400
CCGATGTATT	TGATGGTGAC	CTGGGAATGG	GGGCAGCCAA	440
GGGGCTGCAA	AGCCTCCCCA	CACATGACCC	CAGCCCTCTA	480
CAGCGGTACA	GTGAGGACCC	CACAGTACCC	CTGCCCTCTG	520
AGACTGATGG	CTACGTTGCC	CCCCTGACCT	GCAGCCCCA	560
GCCTGAATAT	GTGAACCAGC	CAGATGTTCG	GCCCCAGCCC	600
CCTTCGCCCC	GAGAGGGCCC	TCTGCCTGCT	GCCCGACCTG	640
CTGGTGCCAC	TCTGGAAAGG	CCCAAGACTC	TCTCCCCAGG	680
GAAGAATGGG	GTCGTCAAAG	ACGTTTTGTC	CTTTGGGGGT	720
GCCGTGGAGA	ACCCCGAGAC	TTGACACCCC	AGGGAGGAGC	760
TGCCCCTCAG	CCCCACCCCTC	CTCCTGCCTT	CAGCCCAGCC	800
TTCGACAACC	TCTATTACTG	GGACCAGGAC	CCACCAAGAGC	840
GGGGGGCTCC	ACCCAGCACC	TTCAAAGGA	CACCTACGGC	880
AGAGAACCCA	GAGTACCTGG	GTCTGGACGT	GCCAGTGTGA	920
AGCCTTAAGG	GCCATATGGT	GAGTGGATGC	CTTGACCCCCA	960
GGCGGGGATG	GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	1000
GCACAGGCCA	ATGCCGTCC	TTCCCCCTGCA	GTGAGTAGTG	1040
ACTGCCCGGG	TGGGATCCCT	GTGACCCCTC	CCCAGTGCCT	1080
CTCCTGGCCC	TGGAAGTTGC	CACTCCAGTG	CCCACCAGCC	1120
TTGTCTTAAT	AAAATAAGT	TGCATCATTT	TGTCTGACTA	1160
GGTGTCTCT	ATAATATTAT	AAGCTTGATA	TCGAATTCTT	1200
TCTCAACGTA	ACACTTACA	GCGGCGCGTC	ATTTGATATG	1240
ATGCGCCCCG	CTTCCCGATA	AGGGAGCAGG	CCAGTAAAAG	1280
CATTACCCGT	GGTGGGGTTC	CCGAGCGGCC	AAAGGGAGCA	1320
GAECTCTAAAT	CTGCCGTCA	CGACTTCGAA	GGTTCGAATC	1360
CTTCCCCCAC	CACCATCACT	TTCAAAAGTC	CGAAAGAATT	1400
CCTGCAGCCC	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1440
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	1480
TGTTACCACT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	1520
TACCGGGTTG	GAATCAAGAC	GATAGTTACC	GGATAAGGCG	1560
CAGCGGTGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	1600
GCTTGGAGCG	AACGACCTAC	ACCGAAGTGA	GATACCTACA	1640
GCGTGAGCAT	TGAGAAAAGCG	CCACGCTTCC	CGAAGGGAGA	1680
AAGGGCGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	1720
GAGAGCGCAC	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	1760

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TCTTTATAGT	CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	1820
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCCTAT	1860
GGAAAAACGC	CAGCAACGCG	GCCGGGGGAT	CCGGAGAGCT	1900
CACTCTAGAT	GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	1940
GAATTTCGG	AGCTATTCA	TTTTCTTTT	CCGTTTTGTG	1980
CAATTTCACT	TATGATAACCG	GCCAATGCTT	GGTTGCTATT	2020
TTGGAAAATC	CCCTTAGGGG	ATGCCCTCA	ACTGGCCCTA	2060
TAAAGGGCCA	GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	2100
TCAAGACAGC	ACGTGGACCT	CGCACAGCCT	CTCCCACAGG	2140
	TACCT			2145

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

GTCTGCCACC ATGGCCTACT CCCCTGC

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(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

TTCTTTGGTG ACCTACCTCT TCGGAATTGC CGAGTC

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(2) INFORMATION FOR SEQ ID NO:25:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1242 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGAGGAGC	CGCAGTCAGA	TCCTAGCGTC	GAGCCCCCTC	40
TGAGTCAGGA	AACATTTC	GACCTATGGA	AACTACTTCC	80
TGAAAACAAC	GTTCTGTCCC	CCTTGCCGTC	CCAAGCAATG	120
GATGATTGTA	TGCTGTCCCC	GGACGATATT	GAACAAATGGT	160
TCACTGAAGA	CCCAGGTCCA	GATGAAGCTC	CCAGAAATGCC	200
AGAGGGCTGCT	CCCCCGCGTGG	CCCCTGCACC	AGCAGCTCCT	240
ACACCGGGCGG	CCCCTGCACC	AGCCCCCTCC	TGGCCCCCTGT	280
CATCTCTGT	CCCTTCCCAG	AAAACCTACC	AGGGCAGCTA	320
CGGTTCCGT	CTGGGCTTCT	TGCATTCTGG	GACAGCCAAG	360
TCTGCCACCA	TGGCCTACTC	CCCTGCGTCT	GTGACTTGCA	400
CGTACTCCCC	TGCCCTCAAC	AAGATGTTT	GCCAACCTGGC	440
CAAGACCTGC	CCTGTGCAGC	TGTGGGTTGA	TTCCACACACC	480
CCGCCCCGGCA	CCCGCGTCCG	CGCCATGGCC	ATCTACAAGC	520
AGTCACAGCA	CATGACGGAG	GTTGTGAGGC	GCTGCCCCCA	560
CCATGAGCGC	TGCTCAGATA	GCGATGGTCT	GGCCCCCTCCT	600
CAGCGCTTTA	TCCGAGTGGA	AGGAAATTG	CGTGTGGAGT	640
ATTGGGATGA	CAGAAACACT	TTTCGACATA	GTGTGGTGGT	680
GCCCTATGAG	CCGCCTGAGG	TTGGCTCTGA	CTGTACCACC	720
ATCCACTACA	ACTACATGTG	TAACAGTTCC	TGCATGGCG	760
GCATGAACCG	GAGGCCCATC	CTCACCATCA	TCACACTGGA	800
AGACTCCAGT	GGTAATCTAC	TGGGACGGAA	CAGCTTGAG	840
GTGCGTGT	GTGCCTGTCC	TGGGAGAGAC	CGGCGCACAG	880
AGGAAGAGAA	TCTCCGCAAG	AAAGGGGAGC	CTCACCAACGA	920
GCTGCCCTCA	GGGAGCACTA	AGCGAGCACT	GCCCAACAAAC	960
ACCAGCTCCT	CTCCCCAGCC	AAAGAAGAAA	CCACTGGATG	1000
GAGAATATT	CACCCCTCAG	ATCCGTGGGC	GTGAGCGCTT	1040
CGAGATGTT	TTTGGTGACC	TACCTCTTCG	GAATTGCCGA	1080
GTCTTCCGAG	AGCTGAATGA	GGCCTTGGAA	CTCAAGGATG	1120
CCCAGGCTGG	GAAGGAGCCA	GGGGGGAGCA	GGGCTCACTC	1160
CAGCCACCTG	AAGTCCAAAA	AGGGTCAGTC	TACCTCCCGC	1200
CATAAAAAC	TCATGTTCAA	GACAGAAGGG	CCTGACTCAG	1240
AC				1242

(2) INFORMATION FOR SEQ ID NO:26:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 608 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCGGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCC	40
CCCTGACGAG	CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	80
TGGCGAAACC	CGACAGGACT	ATAAAAGATAC	CAGGCGTTTC	120
CCCCTGGAAG	CTCCCCTCGTG	CGCTCTCCCTG	TTCCGACCCCT	160
GCCGCTTAC	GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	200
AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	AGGTATCTCA	240
GTTCGGTGTA	GGTCGTTCGC	TCCAAGCTGG	GCTGTGTGCA	280
CGAACCCCCC	GTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	320
AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	CACGACTTAT	360
CGCCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	400
GAGGTATGTA	GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	440
CCTAACTACG	GCTACACTAG	AAGGACAGTA	TTTGGTATCT	480
GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	520
TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	560
GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	CGCAGAAAAAA	600
AAGGATCT				608

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1547 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCGG	120

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CCCTGGACTG	TTGAACGAGG	TGGCGTAGA	CGGTCTGACG	160
ACACGCAAAC	TGGCGGAACG	GTTGGGGTG	CAGCAGCCGG	200
CGCTTACTG	GCACTTCAAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCCA	GGCGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCGTCC	TTCCCCCTGCA	GGATGAGTAG	TGAGTGCCCTC	360
TCCTGGCCCT	GGAAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCTTAATA	AAATTAAGTT	GCATCATTTT	GTCTGACTAG	440
GTGTCTCTA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCCCA	CCACGGGTAA	TGCTTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGCGC	ATCATATCAA	640
ATGACGCGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTC	680
CTGCAGCCCG	CCGCCTTGCT	GGCGTTTTTC	CATAGGCTCC	720
GCCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTCAAG	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACATAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTGGT	1160
ATCTGCGCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTT	TTTGTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	ACTCTAGATG	1320
AGAGAGCAGT	GAGGGAGAGA	CAGAGACTCG	AATTTCGGA	1360
GCTATTTCA	TTTTCTTTTC	CGTTTTGTGC	AATTCACTT	1400
ATGATACCGG	CCAATGCTTG	GTTGCTATTT	TGGAAACTCC	1440
CCTTAGGGGA	TGCCCCCTCAA	CTGGCCCTAT	AAAGGGCCAG	1480
CCTGAGCTGC	AGAGGATTCC	TGCAGAGGAT	CAAGACAGCA	1520
CGTGGACCTC	GCACAGCCTC	TCCCACCA		1547

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1847 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:28:

GGTACCTGCC	ACCATGGCGC	GGATTCTTTA	TCACTGATAA	40
GTTGGTGGAC	ATATTATGTT	TATCAGTGAT	AAAGTGTCAA	80
GCATGACAAA	GTTGCAGCCG	AATACAGTGA	TCCGTGCCGG	120
CCCTGGACTG	TTGAACGAGG	TCGGCGTAGA	CGGTCTGACG	160
ACACGCAAC	TGGCGGAACG	GTTGGGGGTG	CAGCAGCCGG	200
CGCTTACTG	GCACTTCAGG	AACAAGCGGG	CGCCTTAAGG	240
GCCATATGGT	GAGTGGATGC	CTTGACCCCCA	GGCGGGGATG	280
GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	GCACAGGCCA	320
ATGCCCGTCC	TTCCCCCTGCA	GGATGAGTAG	TGAGTGCCCT	360
TCCTGGCCCT	GGAAGTTGCC	ACTCCAGTGC	CCACCAGCCT	400
TGTCTTAATA	AAATTAAGTT	GCATCATTTT	GTCTGACTAG	440
GTGTCTCTA	TAATATTATA	AGCTTGATAT	CGAATTCTTT	480
CGGACTTTG	AAAGTGATGG	TGGTGGGGGA	AGGATTCGAA	520
CCTTCGAAGT	CGATGACGGC	AGATTTAGAG	TCTGCTCCCT	560
TTGGCCGCTC	GGGAACCCC	CCACGGGTAA	TGCTTTTACT	600
GGCCTGCTCC	CTTATCGGGA	AGCGGGGC	ATCATATCAA	640
ATGACCGGCC	GCTGTAAAGT	GTTACGTTGA	GAAAGAATTG	680
CTGCAGCCCG	CCCGCGTTGCT	GGCGTTTTTC	CATAGGCTCC	720
GCCCCCCTGA	CGAGCATCAC	AAAAATCGAC	GCTCAAGTCA	760
GAGGTGGCGA	AACCCGACAG	GACTATAAAAG	ATACCAGGCG	800
TTTCCCCCTG	GAAGCTCCCT	CGTGCCTCT	CCTGTTCCGA	840
CCCTGCCGCT	TACCGGATAC	CTGTCCGCCT	TTCTCCCTTC	880
GGGAAGCGTG	GCGCTTCTC	AATGCTCACG	CTGTAGGTAT	920
CTCAGTTCGG	TGTAGGTCGT	TCGCTCCAAG	CTGGGCTGTG	960
TGCACGAACC	CCCCGTTCA	CCCGACCGCT	GCGCCTTATC	1000
CGGTAACAT	CGTCTTGAGT	CCAACCCGGT	AAGACACGAC	1040
TTATCGCCAC	TGGCAGCAGC	CACTGGTAAC	AGGATTAGCA	1080
GAGCGAGGTA	TGTAGGCGGT	GCTACAGAGT	TCTTGAAGTG	1120
GTGGCCTAAC	TACGGCTACA	CTAGAAGGAC	AGTATTTGGT	1160
ATCTCGCCTC	TGCTGAAGCC	AGTTACCTTC	GGAAAAAGAG	1200
TTGGTAGCTC	TTGATCCGGC	AAACAAACCA	CCGCTGGTAG	1240
CGGTGGTTTT	TTTGTGCA	AGCAGCAGAT	TACGCGCAGA	1280
AAAAAAGGAT	CTGGGGGATC	CGGAGAGCTC	CCAACCGT	1320
GGATGCATGG	ATGAGGGAAA	GGAGGTAAGA	TCTGTAATGA	1400
ATAAGCAGGA	ACTTTGAAGA	CTCAGTGACT	CAGTGAGTAA	1440
TAAAGACTCA	GTGACTTCTG	ATCCTGCTCT	AACTGCCACT	1480
CCTTGTGTC	CCAAGAAAGC	GGCTTCTG	TCTCTGAGGA	1520
GGACCCCTTC	CCTGGAAGGT	AAAACTAAGG	ATGTCAGCAG	1560
AGAAATTTT	CCACCATTGG	TGCTTGGTCA	AAGAGGAAAC	1600
TGATGAGCTC	ACTCTAGATG	AGAGAGCAGT	GAGGGAGAGA	1640
CAGAGACTCG	AATTTCCGGA	GCTATTTCAG	TTTTCTTTTC	1680
CGTTTGTGC	AATTTCACTT	ATGATACCGG	CCAATGCTTG	1720
GTTGCTATTT	TGGAAACTCC	CCTTAGGGGA	TGCCCCCTCAA	1760
CTGGCCCTAT	AAAGGGCCAG	CCTGAGCTGC	AGAGGATTCC	1800
TGCAGAGGAT	CAAGACAGCA	CGTGGACCTC	GCACAGCCTC	1840
TCCCACAA				1847

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTACCTGCC	ACCATGGCGA	AGGGCGAGGA	ACTGTTCACT	40
GGCGTGGTCC	CAATTCTCGT	GGAACTGGAT	GGCGATGTGA	80
ATGGGCACAA	ATTTTCTGTC	AGCGGAGAGG	GTGAAGGTGA	120
TGCCACATAC	GGAAAGCTCA	CCCTGAAATT	CATCTGCACC	160
ACTGGAAAGC	TCCCTGTGCC	ATGGCCAACA	CTGGTCACTA	200
CCTTCACCTA	TGGCGTGCAG	TGCTTTCCA	GATACCCAGA	240
CCATATGAAG	CAGCATGACT	TTTCAAGAG	CGCCATGCC	280
GAGGGCTATG	TGCAGGAGAG	AACCATCTTT	TTCAAAGATG	320
ACGGGAACTA	CAAGACCCGC	GCTGAAGTCA	AGTTCGAAGG	360
TGACACCCCTG	GTGAATAGAA	TCGAGTTGAA	GGGCATTGAC	400
TTTAAGGAAG	ATGGAAACAT	TCTCGGCCAC	AAGCTGGAAT	440
ACAACATATAA	CTCCCACAAT	GTGTACATCA	TGGCCGACAA	480
GCAAAAGAACAT	GGCATCAAGG	TCAACTTCAA	GATCAGACAC	520
AACATTGAGG	ATGGATCCGT	GCAGCTGGCC	GACCATTATC	560
AACAGAACAC	TCCAATCGGC	GACGGCCCTG	TGCTCCTCCC	600
AGACAACCAT	TACCTGTCCA	CCCAGTCTGC	CCTGTCTAAA	640
GATCCAACG	AAAAGAGAGA	CCACATGGTC	CTGCTGGAGT	680
TTGTGACCGC	TGCTGGGATC	ACACATGGCA	TGGACGAGCT	720
GTACAAGTGA	GCGCCTTAAG	GGCCATATGG	TGAGTGGATG	760
CCTTGACCCCC	AGGCGGGGAT	GGGGGAGACC	TGTAGTCAGA	800
GCCCCCGGGC	AGCACAGGCC	AATGCCCGTC	CTTCCCTGTC	840
AGGATGAGTA	GTGAGTGCCT	CTCCTGGCCC	TGGAAGTTGC	880
CACTCCAGTG	CCCACCAGCC	TTGTCTTAAT	AAAATTAAGT	920
TGCATCATTT	TGTCTGACTA	GGTGTCTCT	ATAATATTAT	960
AAGCTTGATA	TCGAATTCTT	TCGGACTTTT	GAAAGTGTATG	1000
GTGGTGGGGG	AAGGATTCGA	ACCTTCGAAG	TCGATGACGG	1040
CAGATTAGA	GTCTGCTCCC	TTTGGCCGCT	CGGGAACCCCC	1080
ACCACGGGTA	ATGCTTTAC	TGGCCTGCTC	CCTTATCGGG	1120
AAGCGGGCG	CATCATATCA	AATGACGCC	CGCTGTAAAG	1160
TGTTACGTTG	AGAAAAGATT	CCTGCAGCCC	GCCGCCTTGC	1200
TGGCGTTTTT	CCATAGGCTC	CGCCCCCCTG	ACGAGCATCA	1240
CAAAAATCGA	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA	1280
GGACTATAAA	GATACCAGGC	GTTCCTCCCT	GGAAAGCTCCC	1320
TCGTGCGCTC	TCCTGTTCCG	ACCCCTGCCGC	TTACCGGATA	1360
CCTGTCCGCC	TTTCTCCCTT	CGGGAAAGCGT	GGCGCTTTCT	1400
CAATGCTCAC	GCTGTAGGTA	TCTCAGTTCG	GTGTAGGTGC	1440
TTCGCTCCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA	1480
GCCCCGACCGC	TGCGCCTTAT	CCGGTAACTA	TCGTCTTGAG	1520
TCCAACCCGG	TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	1560

SEQUENCE DESCRIPTION

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CCACTGGTAA	CAGGATTAGC	AGAGCGAGGT	ATGTAGGC GG	1600
TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	CTACGGCTAC	1640
ACTAGAAGGA	CAGTATTG G	TATCTGCGCT	CTGCTGAAGC	1680
CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG	1720
CAAACAAACC	ACCGCTGGTA	GCGGTGGTTT	TTTGTTTGC	1760
AAGCAGCAGA	TTACGCGCAG	AAAAAAAGGA	TCTGGGGGAT	1800
CCGGAGAGCT	CCCAACGCGT	TGGATGCATG	GATGAGGGAA	1840
AGGAGGTAAG	ATCTGTAATG	AATAAGCAGG	AACTTTGAAG	1880
ACTCAGTGAC	TCAGTGAGTA	ATAAAAGACTC	AGTGACTTCT	1920
GATCCTGTCC	TAACTGCCAC	TCCTTGTG T	CCCAAGAAAAG	1960
CGGCTCCTG	CTCTCTGAGG	AGGACCCCTT	CCCTGGAAGG	2000
TAAAACTAAG	GATGT CAGCA	GAGAAATTTT	TCCACCATTG	2040
GTGCTTGGTC	AAAGAGGAAA	CTGATGAGCT	CACTCTAGAT	2080
GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	GAATTTCCGG	2120
AGCTATTTCA	GT TTTCTTTT	CCGTTTTGTG	CAATTTCACT	2160
TATGATACCG	GCCAATGCTT	GGTTGCTATT	TTGGAAACTC	2200
CCCTTAGGGG	ATGCCCTCA	ACTGGCCCTA	TAAAGGGCCA	2240
GCCTGAGCTG	CAGAGGATT C	CTGCAGAGGA	TCAAGACAGC	2280
ACGTGGACCT	CGCACAGCCT	CTCCCACA		2308

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